

IN THE CLAIMS:

Please amend the claims as follows:

Please cancel renumbered claims 1-24, 30-37, 40-43, 45, 46, 48-50 and 55-57 without prejudice.

1-24. (canceled)

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25. (currently amended) A transgenic plant cell comprising an endogenous nucleotide sequence identical or at least 98% sequence similarity and encoding a polypeptide having 3'-5' exonuclease activity [or substantially similar] to [SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or] SEQ ID NO:23, and wherein said plant cell comprises a mutation in said endogenous nucleotide sequence, or in a regulatory region thereof.

26. (currently amended) The transgenic plant cell of claim 25, wherein the mutation is due to an insertion of a nucleic acid molecule.

27. (currently amended) The transgenic plant cell according to claim [25] 26, wherein the insertion of a nucleic acid molecule comprises one T-DNA border region.

[29] 28. (currently amended) The transgenic plant cell according to claim [25] 27, wherein the insertion comprises a transposable element.

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30-37. (canceled)

38 [39]. (currently amended) A transgenic plant or progeny thereof, or seeds thereof comprising the plant cell of claim 25[, or progeny thereof, or seeds thereof].

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39 [40]. (currently amended) A transgenic plant or progeny thereof, or seeds thereof comprising the plant cell of claim 26[, or progeny thereof, or seeds thereof].

40-42. (canceled)

43 [44]. (canceled)

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44 [45]. (currently amended) [The method according to claim 44] A method for altering the expression in a plant cell or plant of an endogenous nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain, wherein said polypeptide is identical to SEQ ID NO:24,

wherein altering the transcription or translation of said endogenous nucleotide sequence in the plant cell or plant comprises the step of:

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- a) expressing in said plant cell a nucleotide sequence identical or has at least 98% sequence similiarity and encodes a polypeptide having 3'-5' exonuclease activity [or substantially similar] to [SEQ ID NO:1,SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or] SEQ ID NO:23, or a portion thereof, in sense orientation; or
- b) expressing in said plant cell a nucleotide sequence identical or has at least 98% sequence similiarity and encodes a polypeptide having 3'-5' exonuclease activity [or substantially similar] to [SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or] SEQ ID NO:23, or a portion thereof, in anti-sense orientation; or
- c) expressing in said plant cell a sense RNA of a nucleotide sequence identical or has at least 98% sequence similiarity and encodes a polypeptide having 3'-5' exonuclease acitivity [or substantially similar] to [SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, or] SEQ ID NO:23, or a portion thereof, and an anti-sense RNA of said nucleotide sequence identical or has at least 98% sequence similiarity [or substantially similar] to [SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or] SEQ ID NO:23, or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or
- d) expressing in said plant cell a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or has at least 98% sequence similiarity and encodes a polypeptide having 3'-5' exonuclease activity [or substantially similar] to [SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, or] SEQ ID NO:23; or
- e) [modifying by homologous recombination in said plant cell at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or SEQ ID NO:23 or of a regulatory region thereof; or
- f)] expressing in said plant cell a zinc finger protein that is capable of binding to a nucleotide sequence identical or has at least 98% sequence similiarity and encodes a polypeptide having 3'-5' exonuclease activity [or substantially similar] to [SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or] SEQ ID NO:23 or to a regulatory region thereof[; or

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g) introducing into said plant cell a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or SEQ ID NO:23 or a regulatory region thereof; _____
f) modifying by insertional mutagenesis in said plant cell at least one chromosomal copy of the nucleotide sequence identical or having at least 98% sequence similarity and encoding a polypeptide having 3'-5' exonuclease activity to SEQ ID NO:23 or of a regulatory region thereof.

45 [46]. (canceled)

46 [47]. (canceled)

47 [48]. (currently amended) [The method according to claim 47], A method for altering the expression of a nucleotide sequence of interest in a plant cell or plant comprising the steps of:

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a) altering the expression in said plant cell or plant of an endogenous nucleotide sequence of said plant cell that is identical or having at least 98% sequence similarity to SEQ ID NO:23; wherein step a) comprises:

[a]i) expressing in said plant cell or plant a nucleotide sequence identical or has at least 98% sequence similarity and encodes a polypeptide having 3'-5' exonuclease activity [or substantially similar] to [SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, or] SEQ ID NO:23, or a portion thereof, in sense orientation; or

[b]ii) expressing in said plant cell or plant a nucleotide sequence identical or has at least 98% sequence similarity and encodes a polypeptide having 3'-5' exonuclease activity [or substantially similar] to [SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, or] SEQ ID NO:23 or a portion thereof, in anti-sense orientation; or

[c] iii) expressing in said plant cell or plant a sense RNA of a nucleotide sequence identical or has at least 98% sequence similarity and encodes a polypeptide having 3'-5' exonuclease activity [or substantially similar] to [SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, or] SEQ ID NO:23, or a portion thereof, and an anti-sense RNA of said nucleotide sequence that has at least 98% sequence similarity and encodes a polypeptide having 3'-5' exonuclease activity [substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ

ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15 or SEQ ID NO:17, or] SEQ ID NO:23 or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or

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[d] iv) expressing in said plant cell or plant a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or has at least 98% sequence similarity and encodes a polypeptide having 3'-5' exonuclease activity [or substantially similar] to [SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or] SEQ ID NO:23; or

[e) modifying by homologous recombination in said plant cell or plant at least one chromosomal copy of the nucleotide sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or SEQ ID NO:23 or of a regulatory region thereof; or

f] v) expressing in said plant cell or plant a zinc finger protein that is capable of binding to a nucleotide sequence [substantially similar] to [SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or] SEQ ID NO:23 or to a regulatory region thereof; or

g) introducing into said plant cell or plant a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or SEQ ID NO:23 or a regulatory region thereof]

f) modifying by insertional mutagenesis in said plant cell at least one chromosomal copy of the nucleotide sequence identical or having at least 98% sequence similarity and encoding a polypeptide having 3'-5' exonuclease activity to SEQ ID NO:23 or of a regulatory region thereof; and

b) introducing into said plant cell or plant a nucleic acid molecule comprising said nucleotide sequence of interest, wherein the expression of said nucleotide sequence of interest in said plant cell or plant is altered.

48-50. (canceled)

51 [52]. (currently amended) A method for stabilizing the expression of [a] an exogenous nucleotide sequence of interest in a transgenic plant cell or plant comprising the steps of:

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a) obtaining a transgenic plant cell or plant having altered expression [in a plant cell] of an endogenous nucleotide sequence of said plant cell or plant comprising a first expression cassette that encodes a polypeptide comprising a 3'-5' exonuclease domain, and wherein

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said polypeptide is identical [or substantially similar] to an amino acid sequence of [SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, or] SEQ ID NO:24; and

b) introducing into said transgenic plant cell or plant [a] an exogenous nucleotide sequence of interest,

wherein the expression of said exogenous nucleotide sequence of interest in said transgenic plant cell is stabilized as compared to the expression of said nucleotide sequence of interest in a plant cell or plant lacking said first expression cassette.

52 [53]. (currently amended) The method according to claim [52] 51, wherein said endogenous nucleotide sequence is identical or has at least 98% sequence similiarity and encodes a polypeptide having 3'-5' exonuclease activity [or substantially similar] to a nucleotide sequence selected from the group consisting of [SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, or] SEQ ID NO:23.

53 [54].(currently amended) The method according to claim [52] 51, wherein the expression of said endogenous nucleotide sequence is altered by:

- a) expressing in said plant cell a nucleotide sequence or has at least 98% sequence similiarity and encodes a polypeptide having 3'-5' exonuclease activity [substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17 or] SEQ ID NO:23, or a portion thereof, in sense orientation; or
- b) expressing in said plant cell a nucleotide sequence or has at least 98% sequence similiarity and encodes a polypeptide having 3'-5' exonuclease activity [substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or] SEQ ID NO:23, or a portion thereof, in anti-sense orientation; or
- c) expressing in said plant cell a sense RNA of a nucleotide sequence identical or has at least 98% sequence similiarity and encodes a polypeptide having 3'-5' exonuclease activity [or substantially similar] to [SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, or] SEQ ID NO:23 or a portion thereof, and an anti-sense RNA of said nucleotide sequence [substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, or] SEQ ID NO:23 or a portion thereof, wherein said sense and said anti-sense RNAs are capable of forming a double-stranded RNA molecule; or

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- d) expressing in said plant cell a ribozyme capable of specifically cleaving a messenger RNA transcript encoded by a nucleotide sequence identical or has at least 98% sequence similarity and encodes a polypeptide having 3'-5' exonuclease activity [or substantially similar] to [SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13; or] SEQ ID NO:23 or
- e) expressing in said plant cell an aptamer specifically directed to a polypeptide of substantially similar to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:22, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14; or SEQ ID NO:24 or
- f) [modifying by homologous recombination in said plant cell at least one chromosomal copy of the nucleotide sequence identical or substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, or SEQ ID NO:23 or of a regulatory region thereof; or
- g) expressing in said plant cell a zinc finger protein that is capable of binding to a nucleotide sequence substantially similar to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, or SEQ ID NO:23 or to a regulatory region thereof; or]
- f [h]) introducing into said plant cell a chimeric oligonucleotide that is capable of modifying at least one chromosomal copy of the nucleotide sequence that has at least 98% sequence identity and encodes a polypeptide having 3'-5' exonuclease activity [identical or substantially similar] to [SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, or] SEQ ID NO:23 or a regulatory region thereof; or
- g) modifying by insertional mutagenesis in said plant cell at least one chromosomal copy of the nucleotide sequence identical or having at least 98% sequence similarity and encoding a polypeptide having 3'-5' exonuclease activity to SEQ ID NO:23 or of a regulatory region thereof.

54 [55]. (currently amended) The method according to claim 53 [54], wherein the expression [in a plant cell] of said endogenous nucleotide sequence is reduced.

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55-57. (canceled)

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58 [59]. (currently amended) The transgenic [A] plant cell of claim 25, wherein the mutation is a deletion or rearrangement.

59 [60]. (currently amended) [A] The transgenic plant cell of claim 25, wherein the mutation is a point mutation.

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